

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	"20040137569"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:28
L2	0	"200400388888242"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:28
L3	1	"20040038242"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:28
L4	1	"20030232350"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:29
L5	1	"20040213797"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:30
L6	1	"20050025751"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:30
L7	1	"20040137569"	US-PGPUB; USPAT	OR	ON	2006/07/29 12:40
L8	273	dishevelled	US-PGPUB; USPAT	OR	ON	2006/07/29 12:41
L9	10	L8 and (delta-3)	US-PGPUB; USPAT	OR	ON	2006/07/29 12:41

## RESULT 4

## DLL3\_MOUSE

ID DLL3\_MOUSE STANDARD; PRT; 592 AA.  
AC O88516; O35675; Q80W06; Q9QWL9; Q9QWZ7;  
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1998, sequence version 1.  
DT 07-MAR-2006, entry version 51.  
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).  
DE 3).  
GN Name=Dll3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC STRAIN=C57BL/6 X DBA; TISSUE=Embryo;  
RX MEDLINE=97417575; PubMed=9272948;  
RA Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;  
RT "Mouse Dll3: a novel divergent Delta gene which may complement the  
RT function of other Delta homologues during early pattern formation in  
RT the mouse embryo.";  
RL Development 124:3065-3076(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.  
RC STRAIN=129/SvJ;  
RX MEDLINE=98324780; PubMed=9662403; DOI=10.1038/961;  
RA Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,  
RA Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;  
RT "The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation  
RT of early somite boundaries.";  
RL Nat. Genet. 19:274-278(1998).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Neural tube;  
RA Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;  
RT "Specific expression of a divergent type of Delta in a set of earliest  
RT generated neurons including the prospective subplate neurons.";  
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -!- FUNCTION: Inhibits primary neurogenesis. May be required to divert
CC      neurons along a specific differentiation pathway. Play a role in
CC      the formation of somite boundaries during segmentation of the
CC      paraxial mesoderm.
CC  -!- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC      (Probable).
CC  -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC      protein (Probable).
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=2;
CC      IsoId=O88516-1; Sequence=Displayed;
CC      Name=1;
CC      IsoId=O88516-2; Sequence=VSP_001376;
CC  -!- TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
CC      and paraxial mesoderm during embryogenesis.
CC  -!- DOMAIN: The DSL domain is required for binding to the Notch
CC      receptor.
CC  -!- PTM: Ubiquitinated by MIB (MIB1 or MIB2), leading to its
CC      endocytosis and subsequent degradation (By similarity).
CC  -!- DISEASE: A truncating mutation in Dll3 is the cause of the pudgy
CC      (pu) phenotype. Pudgy mice exhibit patterning defects at the
CC      earliest stages of somitogenesis. Adult pudgy mice present severe
CC      vertebral and rib deformities.
CC  -!- SIMILARITY: Contains 1 DSL domain.
CC  -!- SIMILARITY: Contains 6 EGF-like domains.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AF068865; AAC40170.1; -; Genomic_DNA.
DR  EMBL; AF068865; AAC40169.1; -; Genomic_DNA.
DR  EMBL; Y11895; CAA72637.1; -; mRNA.
DR  EMBL; AB013440; BAA33716.1; -; mRNA.
DR  EMBL; BC052002; AAH52002.1; -; mRNA.
DR  HSSP; P00740; 1EDM.
DR  Ensembl; ENSMUSG00000003436; Mus musculus.
DR  MGI; MGI:1096877; Dll3.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0016021; C:integral to membrane; TAS.
DR  GO; GO:0005112; F:Notch binding; NAS.
DR  GO; GO:0001709; P:cell fate determination; NAS.
DR  GO; GO:0007386; P:compartment specification; IMP.
DR  GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
DR  GO; GO:0007399; P:neurogenesis; NAS.
DR  GO; GO:0007219; P:Notch signaling pathway; NAS.
DR  GO; GO:0001501; P:skeletal development; IMP.
DR  InterPro; IPR001774; DSL.
DR  InterPro; IPR006210; EGF.
DR  InterPro; IPR001438; EGF_2.
DR  InterPro; IPR000742; EGF_3.
DR  InterPro; IPR001881; EGF_Ca_bd.
DR  InterPro; IPR013111; EGF_extracell.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR013032; EGF_like_reg.
DR  InterPro; IPR011651; Notch_ligand_N.
DR  Pfam; PF00008; EGF; 5.
DR  Pfam; PF07974; EGF_2; 1.

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DR Pfam; PF07657; MNNL; 1.  
 DR PRINTS; PR00010; EGF BLOOD.  
 DR SMART; SM00181; EGF; 6.  
 DR PROSITE; PS51051; DSL; FALSE\_NEG.  
 DR PROSITE; PS00022; EGF\_1; 6.  
 DR PROSITE; PS01186; EGF\_2; 6.  
 DR PROSITE; PS50026; EGF\_3; 6.  
 KW Alternative splicing; Developmental protein; Differentiation;  
 KW EGF-like domain; Membrane; Notch signaling pathway; Repeat; Signal;  
 KW Transmembrane; Ubl conjugation.  
 FT SIGNAL 1 32 Potential.  
 FT CHAIN 33 592 Delta-like protein 3.  
 FT /FTId=PRO\_0000007510.  
 FT TOPO\_DOM 33 490 Extracellular (Potential).  
 FT TRANSMEM 491 511 Potential.  
 FT TOPO\_DOM 512 592 Cytoplasmic (Potential).  
 FT DOMAIN 174 213 DSL.  
 FT DOMAIN 214 247 EGF-like 1.  
 FT DOMAIN 272 308 EGF-like 2.  
 FT DOMAIN 310 349 EGF-like 3.  
 FT DOMAIN 351 387 EGF-like 4.  
 FT DOMAIN 389 425 EGF-like 5.  
 FT DOMAIN 427 463 EGF-like 6.  
 FT DISULFID 218 229 By similarity.  
 FT DISULFID 222 235 By similarity.  
 FT DISULFID 237 246 By similarity.  
 FT DISULFID 276 287 By similarity.  
 FT DISULFID 281 296 By similarity.  
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 FT DISULFID 319 337 By similarity.  
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 FT DISULFID 355 366 By similarity.  
 FT DISULFID 360 375 By similarity.  
 FT DISULFID 377 386 By similarity.  
 FT DISULFID 393 404 By similarity.  
 FT DISULFID 398 413 By similarity.  
 FT DISULFID 415 424 By similarity.  
 FT DISULFID 431 442 By similarity.  
 FT DISULFID 436 451 By similarity.  
 FT DISULFID 453 462 By similarity.  
 FT VARSPLIC 585 592 DWLIQVLF -> A (in isoform 1).  
 FT /FTId=VSP\_001376.  
 FT CONFLICT 94 94 E -> K (in Ref. 3).  
 FT CONFLICT 401 401 G -> A (in Ref. 1).  
 SQ SEQUENCE 592 AA; 62069 MW; 1A84F8022E7E7DCC CRC64;

Query Match 83.6%; Score 2729; DB 1; Length 592;  
 Best Local Similarity 82.8%; Pred. No. 1.2e-163;  
 Matches 485; Conservative 33; Mismatches 62; Indels 6; Gaps 3;

QY 1 MVSPRMSGLLSQTIVILALIFLPQTRPAGVFELQIHSFGPGPGPGAPRSPCSARLPCLRLF 60  
 ||| ::| ||||:|||| : ||| ||||| ||||| ||| |||||: || |||||  
 Db 1 MVSLQVSP-LSQTLILAFLLPQALPAGVFELQIHSFGPGPGGLGTPRSPCNARGPCRLFF 58  
 QY 61 RVCLKPGLSEEAESPALGAALSARGPVYTEQPAPDLPLPDGLLQVPFRDAWPGTF 120  
 |||||:|: || ||||| ||||| || | |||||:|: ||||| |||||  
 Db 59 RVCLKPGVSQEATESLALGAALSTSVPVYTEHPGESAAALPLPDGLVVRVPFRDAWPGTF 118  
 QY 121 SFIIETWREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAWELRCSYRARCEP 180  
 | :|||:|: ||||:|||| ||||| |||||:| ||| |||||

Db 119 SLVIETWREQLGEHAGGPAWNLLARVVGRRRLAAGGPWARDVQRTGTWELHFSYRARCEP 178

Qy 181 PAVGTACTRLCRPRSAPSRGPGLRPCAPLEDE----SVCRAGCSPEHGFCEQPGECRCL 236  
||| || ||| ||||| ||||| ||| ||| ||||| :||| |||||

Db 179 PAVGAACARLCRSRSAPSRGPGLRPCTFFPDECEAPSVCRPGCSPEHGYCEEPDECRL 238

Qy 237 EGWTGPLCTVPVSTSSCLSPRGPSATTGCLVPGPGPCDGNPCANGGSCSETPRSFECTC 296  
||| ||||| ||||| : || ||| : ||||| : ||||| : ||||| : |||||

Db 239 EGWTGPLCTVPVSTSSCLNSRVPGPASTGCLLPGPGPCDGNPCANGGSCSETSGSFECAC 298

Qy 297 PRGFYGLRCEVSGVTCADGPCFNGGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQ 356  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 299 PRGFYGLRCEVSGVTCADGPCFNGGLCVGGEDPDSAYVCHCPPGFQGSNCEKRVDRCSLQ 358

Qy 357 PCRNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGAHRCSCALG 416  
|| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

Db 359 PCQNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGSRRCSALG 418

Qy 417 FGGRDCRERADPCAARPCAHHGRCYAHFSGLVACAPGYMGARCEFPVHPDGASALPAAP 476  
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Db 419 FGGRDCRERADPCASRPCAHHGRCYAHFSGLVACAPGYMGVRCEFAVRPDGADAVPAAP 478

Qy 477 PGLRPGDPQRYLLPPALGLLVAAGVAGAALLLVHVRRRGHSQDAGSRLLAGTPEPSVHAL 536  
||| ||||| : ||||| ||||| : ||||| : ||||| ||| : ||| : ||| |||||

Db 479 RGLRQADPQRFLLPPALGLLVAAGLAGAALLVIHVRRRGPGQDTGTRLLSGTREPSVHTL 538

Qy 537 PDALNNLRTQEGSGDGPSSSVDNRPEDVDPQGIYVISAPSIYARE 582  
||| ||||| : ||||| ||| ||| : ||| |||||

Db 539 PDALNNLRLQDGAGDGPSSADWNHPEDGDSRSIYVIPAPSIYARE 584

This page gives you Search Results detail for the Application 10644548 and Search Result us-10-644-548-2.rag.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:23:21 ; Search time 198 Seconds  
(without alignments)  
1346.248 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3263	100.0	583	4 AAB71740	Aab71740 Human Not
2	3246	99.5	587	5 AAU91338	Aau91338 Human nov
3	3237	99.2	587	4 AAM93686	Aam93686 Human pol
4	3237	99.2	587	8 ADL31553	Adl31553 Human pro
5	3231	99.0	618	6 ABR58644	Abr58644 Human can
6	3231	99.0	618	6 ABP97825	Abp97825 Amino aci

7	3231	99.0	618	6	ABU55878	Abu55878	Human	not
8	3231	99.0	618	6	AAE34034	Aae34034	Human	not
9	3231	99.0	618	6	ABP72567	Abp72567	Human	Not
10	3231	99.0	618	6	ABR61826	Abr61826	Human	del
11	3231	99.0	618	7	ABU63729	Abu63729	Human	Not
12	3231	99.0	618	7	ADN38932	Adn38932	Cancer/an	
13	3231	99.0	618	8	ADK00014	Adk00014	Human	Not
14	3231	99.0	618	8	ADM41512	Adm41512	Human	del
15	3231	99.0	618	8	ADL73026	Adl73026	Human	Not
16	3231	99.0	618	8	ADM76012	Adm76012	Human	Del
17	3231	99.0	618	8	ADQ14405	Adq14405	Human	Del
18	3231	99.0	618	8	ADR20593	Adr20593	Human	Not
19	3231	99.0	618	8	ADR41795	Adr41795	Human	del
20	3231	99.0	618	8	ABM82106	Abm82106	Tumour-as	
21	3231	99.0	618	8	ADR89381	Adr89381	Human	Del
22	3231	99.0	618	8	ADS75457	Ads75457	Human	Del
23	3231	99.0	618	9	ADX58106	Adx58106	Amino aci	
24	3231	99.0	618	9	ADX70417	Adx70417	Human	Del
25	3231	99.0	618	9	AEB77853	Aeb77853	Human	not
26	3231	99.0	1009	8	ADU02432	Adu02432	Novel	hum
27	3222	98.7	618	7	ABR61755	Abr61755	Human	del
28	3210	98.4	582	3	AAAY59442	Aay59442	Full leng	
29	3110	95.3	561	3	AAAY59441	Aay59441	Human	del
30	2707	83.0	589	8	ADR88259	Adr88259	Rattus	no
31	2707	83.0	589	8	ADR88256	Adr88256	Rattus	no
32	2613	80.1	464	3	AAAY59440	Aay59440	Human	del
33	2355	72.2	969	4	ABG29063	Abg29063	Novel	hum
34	1267	38.8	323	3	AAB32417	Aab32417	Human	sec
35	1019	31.2	188	3	AAAY59439	Aay59439	Human	del
36	977.5	30.0	723	8	ADR89380	Adr89380	Human	Del
37	977.5	30.0	740	2	AAW00876	Aaw00876	C-Delta-1	
38	975.5	29.9	723	3	AAAY79032	Aay79032	Human	del
39	975.5	29.9	723	6	ABP97824	Abp97824	Amino aci	
40	975.5	29.9	723	6	ABP72566	Abp72566	Human	Not
41	975.5	29.9	723	6	ABR61825	Abr61825	Human	del
42	975.5	29.9	723	7	ABR61754	Abr61754	Human	del
43	975.5	29.9	723	7	ABU63728	Abu63728	Human	Not
44	975.5	29.9	723	8	ADK00013	Adk00013	Human	Not
45	975.5	29.9	723	8	ADM41511	Adm41511	Human	del

This page gives you Search Results detail for the Application 10644548 and Search Result us-10-644-548-2.ra1.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:32:11 ; Search time 51 Seconds  
(without alignments)  
1000.595 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3263	100.0	583	2	US-09-641-612-2	Sequence 2, Appli
2	2712	83.1	585	2	US-09-641-612-5	Sequence 5, Appli
3	1122.5	34.4	642	2	US-08-872-855-10	Sequence 10, Appl
4	977.5	30.0	728	2	US-08-981-392-2	Sequence 2, Appli
5	977.5	30.0	728	2	US-09-908-322-2	Sequence 2, Appli
6	971.5	29.8	728	2	US-09-310-685-11	Sequence 11, Appl
7	968	29.7	729	2	US-08-872-855-8	Sequence 8, Appli
8	967.5	29.7	723	2	US-09-068-740A-9	Sequence 9, Appli
9	967.5	29.7	723	2	US-09-423-753-27	Sequence 27, Appl



10	967.5	29.7	723	3	US-10-241-476-27	Sequence 27, Appl
11	961.5	29.5	702	2	US-09-068-740A-4	Sequence 4, Appli
12	961.5	29.5	723	2	US-09-641-612-6	Sequence 6, Appli
13	952.5	29.2	520	2	US-09-068-740A-3	Sequence 3, Appli
14	942.5	28.9	722	2	US-09-310-685-14	Sequence 14, Appl
15	939.5	28.8	722	2	US-08-981-392-12	Sequence 12, Appl
16	939.5	28.8	722	2	US-09-908-322-12	Sequence 12, Appl
17	933	28.6	713	2	US-08-872-855-5	Sequence 5, Appli
18	922.5	28.3	720	2	US-08-872-855-4	Sequence 4, Appli
19	916.5	28.1	721	2	US-08-872-855-7	Sequence 7, Appli
20	916.5	28.1	721	2	US-08-981-392-5	Sequence 5, Appli
21	916.5	28.1	721	2	US-09-908-322-5	Sequence 5, Appli
22	907.5	27.8	721	2	US-09-310-685-12	Sequence 12, Appl
23	898	27.5	685	2	US-08-872-855-2	Sequence 2, Appli
24	898	27.5	685	2	US-09-423-753-25	Sequence 25, Appl
25	898	27.5	685	2	US-09-641-612-7	Sequence 7, Appli
26	898	27.5	685	3	US-10-241-476-25	Sequence 25, Appl
27	895	27.4	717	2	US-08-872-855-9	Sequence 9, Appli
28	888	27.2	659	2	US-09-423-753-3	Sequence 3, Appli
29	888	27.2	659	3	US-10-241-476-3	Sequence 3, Appli
30	859.5	26.3	500	2	US-09-423-753-2	Sequence 2, Appli
31	859.5	26.3	500	3	US-10-241-476-2	Sequence 2, Appli
32	673	20.6	833	1	US-08-264-534-6	Sequence 6, Appli
33	673	20.6	833	1	US-08-083-590A-2	Sequence 2, Appli
34	673	20.6	833	1	US-08-465-500-6	Sequence 6, Appli
35	673	20.6	833	1	US-08-346-126-6	Sequence 6, Appli
36	673	20.6	833	1	US-08-346-128-6	Sequence 6, Appli
37	673	20.6	833	2	US-08-532-384-2	Sequence 2, Appli
38	673	20.6	833	2	US-08-893-828-6	Sequence 6, Appli
39	670	20.5	830	2	US-08-872-855-11	Sequence 11, Appl
40	666.5	20.4	832	2	US-08-981-392-6	Sequence 6, Appli
41	666.5	20.4	832	2	US-09-908-322-6	Sequence 6, Appli
42	664	20.3	833	2	US-09-310-685-2	Sequence 2, Appli
43	649.5	19.9	1193	1	US-08-400-159-10	Sequence 10, Appl
44	649.5	19.9	1193	2	US-08-611-729A-10	Sequence 10, Appl
45	649.5	19.9	1193	2	US-09-195-524-10	Sequence 10, Appl

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:33:01 ; Search time 185 Seconds  
(without alignments)  
1459.753 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3263	100.0	583	4	US-10-644-548-2	Sequence 2, Appli
2	3246	99.5	587	4	US-10-343-348-32	Sequence 32, Appl
3	3231	99.0	618	4	US-10-295-027-250	Sequence 250, App
4	3231	99.0	618	4	US-10-763-362-41	Sequence 41, Appl
5	3231	99.0	618	5	US-10-765-727-18	Sequence 18, Appl
6	3231	99.0	618	5	US-10-846-989-52	Sequence 52, Appl
7	3231	99.0	618	5	US-10-764-415B-35	Sequence 35, Appl
8	3231	99.0	618	5	US-10-845-834A-52	Sequence 52, Appl
9	3231	99.0	618	5	US-10-899-422-31	Sequence 31, Appl
10	3231	99.0	618	5	US-10-958-784-41	Sequence 41, Appl

11	3231	99.0	618	6	US-11-078-735-18	Sequence 18, Appl
12	3231	99.0	618	6	US-11-050-346-63	Sequence 63, Appl
13	3231	99.0	618	6	US-11-103-077-18	Sequence 18, Appl
14	3231	99.0	618	6	US-11-058-066-18	Sequence 18, Appl
15	2712	83.1	585	4	US-10-644-548-5	Sequence 5, Appli
16	2707	83.0	589	4	US-10-731-741-2	Sequence 2, Appli
17	2707	83.0	589	4	US-10-731-741-5	Sequence 5, Appli
18	2355	72.2	969	5	US-10-450-763-59422	Sequence 59422, A
19	1267	38.8	323	6	US-11-240-769-103	Sequence 103, App
20	1122.5	34.4	642	4	US-10-417-719-10	Sequence 10, Appl
21	978.5	30.0	942	4	US-10-763-362-40	Sequence 40, Appl
22	978.5	30.0	942	5	US-10-845-834A-51	Sequence 51, Appl
23	977.5	30.0	728	3	US-09-908-322-2	Sequence 2, Appli
24	977.5	30.0	728	3	US-09-783-931-2	Sequence 2, Appli
25	975.5	29.9	723	4	US-10-731-741-1	Sequence 1, Appli
26	975.5	29.9	723	5	US-10-723-860-2752	Sequence 2752, Ap
27	975.5	29.9	723	5	US-10-765-727-17	Sequence 17, Appl
28	975.5	29.9	723	5	US-10-846-989-51	Sequence 51, Appl
29	975.5	29.9	723	5	US-10-764-415B-34	Sequence 34, Appl
30	975.5	29.9	723	5	US-10-899-422-30	Sequence 30, Appl
31	975.5	29.9	723	5	US-10-958-784-40	Sequence 40, Appl
32	975.5	29.9	723	6	US-11-078-735-17	Sequence 17, Appl
33	975.5	29.9	723	6	US-11-050-346-62	Sequence 62, Appl
34	975.5	29.9	723	6	US-11-103-077-17	Sequence 17, Appl
35	975.5	29.9	723	6	US-11-058-066-17	Sequence 17, Appl
36	973	29.8	864	5	US-10-812-144-2	Sequence 2, Appli
37	973	29.8	864	5	US-10-846-989-5	Sequence 5, Appli
38	973	29.8	864	5	US-10-845-834A-5	Sequence 5, Appli
39	973	29.8	864	5	US-10-899-422-50	Sequence 50, Appl
40	973	29.8	864	5	US-10-958-784-7	Sequence 7, Appli
41	973	29.8	864	6	US-11-050-346-10	Sequence 10, Appl
42	973	29.8	864	6	US-11-103-077-29	Sequence 29, Appl
43	971.5	29.8	728	5	US-10-877-563-11	Sequence 11, Appl
44	971.5	29.8	728	6	US-11-022-478-11	Sequence 11, Appl
45	969.5	29.7	723	4	US-10-731-741-3	Sequence 3, Appli

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:33:56 ; Search time 17 Seconds  
(without alignments)  
433.587 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	453.5	13.9	737	6	US-10-196-749-38 Sequence 38, Appl
2	453.5	13.9	737	7	US-11-296-092-15 Sequence 15, Appl
3	429.5	13.2	1523	6	US-10-196-749-290 Sequence 290, App
4	375	11.5	1450	7	US-11-217-997-6 Sequence 6, Appli
5	361	11.1	1398	7	US-11-217-997-4 Sequence 4, Appli
6	361	11.1	1404	7	US-11-217-997-2 Sequence 2, Appli
7	361	11.1	1547	7	US-11-217-997-22 Sequence 22, Appl
8	361	11.1	1577	7	US-11-217-997-16 Sequence 16, Appl

9	361	11.1	1577	7	US-11-217-997-20	Sequence 20, Appl
10	361	11.1	1594	7	US-11-217-997-18	Sequence 18, Appl
11	361	11.1	1620	7	US-11-217-997-42	Sequence 42, Appl
12	361	11.1	1653	7	US-11-217-997-40	Sequence 40, Appl
13	358.5	11.0	1418	7	US-11-217-997-38	Sequence 38, Appl
14	354.5	10.9	1403	7	US-11-217-997-12	Sequence 12, Appl
15	347	10.6	4590	6	US-10-505-928-569	Sequence 569, App
16	335.5	10.3	1198	7	US-11-217-997-14	Sequence 14, Appl
17	327	10.0	575	7	US-11-217-997-32	Sequence 32, Appl
18	318.5	9.8	259	7	US-11-217-997-34	Sequence 34, Appl
19	297.5	9.1	491	7	US-11-217-997-30	Sequence 30, Appl
20	297	9.1	1821	6	US-10-505-928-451	Sequence 451, App
21	281	8.6	342	7	US-11-038-753-1	Sequence 1, Appli
22	269.5	8.3	233	7	US-11-321-421-110	Sequence 110, App
23	260	8.0	575	6	US-10-511-937-2625	Sequence 2625, Ap
24	256.5	7.9	567	7	US-11-246-999-50	Sequence 50, Appl
25	254.5	7.8	472	7	US-11-217-997-26	Sequence 26, Appl
26	252.5	7.7	724	7	US-11-293-697-3263	Sequence 3263, Ap
27	244	7.5	494	7	US-11-246-999-30	Sequence 30, Appl
28	241	7.4	439	7	US-11-293-697-2765	Sequence 2765, Ap
29	241	7.4	4391	7	US-11-183-325-56	Sequence 56, Appl
30	238	7.3	469	7	US-11-246-999-41	Sequence 41, Appl
31	233	7.1	2026	6	US-10-505-928-831	Sequence 831, App
32	231.5	7.1	5738	6	US-10-505-928-150	Sequence 150, App
33	226	6.9	1597	7	US-11-297-134-61	Sequence 61, Appl
34	220.5	6.8	495	6	US-10-511-814-5	Sequence 5, Appli
35	219	6.7	1435	6	US-10-196-749-581	Sequence 581, App
36	218	6.7	1300	6	US-10-196-749-269	Sequence 269, App
37	217.5	6.7	509	6	US-10-196-749-52	Sequence 52, Appl
38	216.5	6.6	1743	6	US-10-196-749-451	Sequence 451, App
39	215.5	6.6	3396	6	US-10-505-928-449	Sequence 449, App
40	213.5	6.5	4440	6	US-10-196-749-525	Sequence 525, App
41	209.5	6.4	1193	6	US-10-505-928-537	Sequence 537, App
42	204.5	6.3	636	6	US-10-521-401A-3	Sequence 3, Appli
43	201.5	6.2	1776	6	US-10-933-854-3	Sequence 3, Appli
44	198.5	6.1	798	6	US-10-511-937-2445	Sequence 2445, Ap
45	194.5	6.0	448	6	US-10-196-749-408	Sequence 408, App

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:27:11 ; Search time 43 Seconds  
(without alignments)  
1304.520 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	977.5	30.0	728	2	I50719	C-Delta-1 - chicke
2	942.5	28.9	722	2	I48324	DELTA-like 1 - mou
3	898	27.5	685	2	JC7570	Delta-4 protein -
4	882	27.0	686	2	JC7569	Delta-4 protein -
5	673	20.6	833	2	S19087	gene Delta protein
6	666.5	20.4	832	2	A31246	neurogenic protein
7	666.5	20.4	880	2	S00670	neurogenic repetit
8	637.5	19.5	1220	2	A56136	jagged protein pre
9	590.5	18.1	2318	2	S45306	notch 3 protein -
10	588.5	18.0	2321	2	S78549	notch3 protein - h
11	588	18.0	1408	2	S16148	gene serrate prote
12	566	17.3	1064	2	A40136	fibropellin Ia - s

13	558	17.1	2471	2	A49128	cell-fate determin
14	552	16.9	1203	2	A49175	Notch B protein -
15	544	16.7	1964	2	T09059	notch4 - mouse
16	538.5	16.5	2703	1	A24420	notch protein - fr
17	537	16.5	2352	2	T30201	Notch homolog prot
18	525.5	16.1	2437	2	S42612	transmembrane prot
19	513.5	15.7	2524	2	A35844	Xotch protein - Af
20	512	15.7	2531	2	T31070	notch homolog - se
21	510.5	15.6	2555	2	A40043	notch protein homo
22	504	15.4	2531	2	S18188	notch protein homo
23	500.5	15.3	2531	2	A46019	notch-1 protein -
24	494	15.1	570	2	A48836	fibropellin C prec
25	487.5	14.9	861	2	A48825	Notch homolog Motc
26	486	14.9	473	2	A56175	adhesive plaque pr
27	466	14.3	2139	2	A35672	crumbs protein - f
28	437	13.4	387	2	B49175	Notch A protein -
29	434.5	13.3	385	2	S53718	homeotic protein d
30	433.5	13.3	1523	2	T13953	MEGF5 protein - ra
31	432	13.2	1372	2	T25933	hypothetical prote
32	430.5	13.2	383	2	S53716	delta-like homeoti
33	428.5	13.1	1531	2	T42218	slit-1 protein hom
34	426.5	13.1	385	2	A54785	preadipocyte facto
35	421.5	12.9	1687	2	T30176	EGF repeat transme
36	415.5	12.7	1025	2	T42626	secreted leucine-r
37	405.5	12.4	1429	2	S06434	homeotic protein l
38	401	12.3	1469	2	B36665	slit protein 2 pre
39	401	12.3	1480	2	A36665	slit protein 1 pre
40	396	12.1	308	2	JC7125	epidermal growth f
41	392	12.0	1722	2	E89753	protein F11C7.4 [i
42	383	11.7	601	2	D89711	protein F40E10.4 [
43	383	11.7	601	2	T22025	hypothetical prote
44	362	11.1	1574	2	T13954	MEGF6 protein - ra
45	358.5	11.0	1295	2	A32901	glp1 protein precu

This page gives you Search Results detail for the Application 10644548 and Search Result us-10-644-548-2.rup.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:23:41 ; Search time 300 Seconds  
(without alignments)  
1797.614 Million cell updates/sec

Title: US-10-644-548-2  
Perfect score: 3263  
Sequence: 1 MVSPRMSGLLSQTVILALIF.....DVDPQGIYVISAPSIYAREA 583

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3237	99.2	587	2 Q8NBS4_HUMAN	Q8nbs4 homo sapien
2	3231	99.0	618	1 DLL3_HUMAN	Q9nyj7 homo sapien
3	2733	83.8	585	2 Q3UND5_MOUSE	Q3und5 mus musculu
4	2729	83.6	592	1 DLL3_MOUSE	O88516 mus musculu
5	2707	83.0	589	1 DLL3_RAT	O88671 rattus norv
6	1132.5	34.7	642	2 Q7ZXT4_XENLA	Q7zxt4 xenopus lae
7	1130.5	34.6	642	2 P79941_XENLA	P79941 xenopus lae
8	1083.5	33.2	664	1 DLLC_BRARE	Q9iat6 brachydanio
9	1073	32.9	615	1 DLLB_BRARE	O57409 brachydanio
10	977.5	30.0	728	2 Q90656_CHICK	Q90656 gallus gall
11	975.5	29.9	723	1 DLL1_HUMAN	O00548 homo sapien
12	949	29.1	714	1 DLL1_RAT	P97677 rattus norv
13	942.5	28.9	722	1 DLL1_MOUSE	Q61483 mus musculu
14	942.5	28.9	722	2 Q6PFV7_MOUSE	Q6pfv7 mus musculu



15	916.5	28.1	721	2	Q91902_XENLA	Q91902 xenopus lae
16	910.5	27.9	726	2	Q8AW87_CYNPY	Q8aw87 cynops pyrr
17	903.5	27.7	772	1	DLLA_BRARE	Q6di48 brachydanio
18	898	27.5	685	1	DLL4_HUMAN	Q9nr61 homo sapien
19	898	27.5	685	2	Q3KP23_HUMAN	Q3kp23 homo sapien
20	895	27.4	717	1	DLLD_BRARE	Q8uwj4 brachydanio
21	888	27.2	686	1	DLL4_MOUSE	Q9ji71 mus musculu
22	882	27.0	686	2	Q9DBU9_MOUSE	Q9dbu9 mus musculu
23	853.5	26.2	669	2	Q4SC13_TETNG	Q4sc13 tetraodon n
24	808	24.8	645	2	Q5RGG6_BRARE	Q5rgg6 brachydanio
25	801	24.5	665	2	Q5SPB5_BRARE	Q5spb5 brachydanio
26	795	24.4	658	2	Q4RLS7_TETNG	Q4rls7 tetraodon n
27	765	23.4	684	2	Q8I498_CUPSA	Q8i498 cupiennius
28	711	21.8	777	2	Q4T963_TETNG	Q4t963 tetraodon n
29	696.5	21.3	1216	2	Q90Y55_BRARE	Q90y55 brachydanio
30	692.5	21.2	1216	2	Q5TZK7_BRARE	Q5tzk7 brachydanio
31	690.5	21.2	452	2	Q5ISL2_MACFA	Q5isl2 macaca fasc
32	678.5	20.8	1254	2	Q90Y56_BRARE	Q90y56 brachydanio
33	676.5	20.7	509	2	Q7Q0M5_ANOGA	Q7q0m5 anopheles g
34	674.5	20.7	1242	1	JAG1A_BRARE	Q90y57 brachydanio
35	674.5	20.7	1254	2	Q5TZK8_BRARE	Q5tzk8 brachydanio
36	674.5	20.7	1254	2	Q9YHU2_BRARE	Q9yhu2 brachydanio
37	673	20.6	794	2	Q8T4P0_LYTVA	Q8t4p0 lytechinus
38	673	20.6	833	1	DL_DROME	P10041 drosophila
39	660	20.2	807	2	Q8MP01_HALRO	Q8mp01 halocynthia
40	655.5	20.1	1128	2	Q4S6G8_TETNG	Q4s6g8 tetraodon n
41	655	20.1	1213	1	JAG1B_BRARE	Q90y54 brachydanio
42	654	20.0	611	2	Q4SZZ8_TETNG	Q4szz8 tetraodon n
43	653	20.0	1247	1	JAG2_MOUSE	Q9qye5 mus musculu
44	649.5	19.9	1193	2	Q90819_CHICK	Q90819 gallus gall
45	649.5	19.9	1238	1	JAG2_HUMAN	Q9y219 homo sapien

RESULT 4

DLL3\_MOUSE

ID DLL3\_MOUSE STANDARD; PRT; 592 AA.  
AC O88516; O35675; Q80W06; Q9QWL9; Q9QWZ7;  
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1998, sequence version 1.  
DT 07-MAR-2006, entry version 51.  
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).  
DE 3).  
GN Name=Dll3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC STRAIN=C57BL/6 X DBA; TISSUE=Embryo;  
RX MEDLINE=97417575; PubMed=9272948;  
RA Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;  
RT "Mouse Dll3: a novel divergent Delta gene which may complement the  
RT function of other Delta homologues during early pattern formation in  
RT the mouse embryo.";  
RL Development 124:3065-3076(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.  
RC STRAIN=129/SvJ;  
RX MEDLINE=98324780; PubMed=9662403; DOI=10.1038/961;  
RA Kusumi K., Sun E.S., Kerrebrock A.W., Bronson R.T., Chi D.-C.,  
RA Bulotsky M.S., Spencer J.B., Birren B.W., Frankel W.N., Lander E.S.;  
RT "The mouse pudgy mutation disrupts Delta homologue Dll3 and initiation  
RT of early somite boundaries.";  
RL Nat. Genet. 19:274-278(1998).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Neural tube;  
RA Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;  
RT "Specific expression of a divergent type of Delta in a set of earliest  
RT generated neurons including the prospective subplate neurons.";  
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -!- FUNCTION: Inhibits primary neurogenesis. May be required to divert
CC      neurons along a specific differentiation pathway. Play a role in
CC      the formation of somite boundaries during segmentation of the
CC      paraxial mesoderm.
CC  -!- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC      (Probable).
CC  -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC      protein (Probable).
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=2;
CC      IsoId=O88516-1; Sequence=Displayed;
CC      Name=1;
CC      IsoId=O88516-2; Sequence=VSP_001376;
CC  -!- TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm
CC      and paraxial mesoderm during embryogenesis.
CC  -!- DOMAIN: The DSL domain is required for binding to the Notch
CC      receptor.
CC  -!- PTM: Ubiquitinated by MIB (MIB1 or MIB2), leading to its
CC      endocytosis and subsequent degradation (By similarity).
CC  -!- DISEASE: A truncating mutation in Dll3 is the cause of the pudgy
CC      (pu) phenotype. Pudgy mice exhibit patterning defects at the
CC      earliest stages of somitogenesis. Adult pudgy mice present severe
CC      vertebral and rib deformities.
CC  -!- SIMILARITY: Contains 1 DSL domain.
CC  -!- SIMILARITY: Contains 6 EGF-like domains.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AF068865; AAC40170.1; -; Genomic_DNA.
DR  EMBL; AF068865; AAC40169.1; -; Genomic_DNA.
DR  EMBL; Y11895; CAA72637.1; -; mRNA.
DR  EMBL; AB013440; BAA33716.1; -; mRNA.
DR  EMBL; BC052002; AAH52002.1; -; mRNA.
DR  HSSP; P00740; 1EDM.
DR  Ensembl; ENSMUSG00000003436; Mus musculus.
DR  MGI; MGI:1096877; Dll3.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0016021; C:integral to membrane; TAS.
DR  GO; GO:0005112; F:Notch binding; NAS.
DR  GO; GO:0001709; P:cell fate determination; NAS.
DR  GO; GO:0007386; P:compartment specification; IMP.
DR  GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
DR  GO; GO:0007399; P:neurogenesis; NAS.
DR  GO; GO:0007219; P:Notch signaling pathway; NAS.
DR  GO; GO:0001501; P:skeletal development; IMP.
DR  InterPro; IPR001774; DSL.
DR  InterPro; IPR006210; EGF.
DR  InterPro; IPR001438; EGF_2.
DR  InterPro; IPR000742; EGF_3.
DR  InterPro; IPR001881; EGF_Ca_bd.
DR  InterPro; IPR013111; EGF_extracell.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR013032; EGF_like_reg.
DR  InterPro; IPR011651; Notch_ligand_N.
DR  Pfam; PF00008; EGF; 5.
DR  Pfam; PF07974; EGF_2; 1.

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DR      Pfam; PF07657; MNNL; 1.
DR      PRINTS; PR00010; EGFBL00D.
DR      SMART; SM00181; EGF; 6.
DR      PROSITE; PS51051; DSL; FALSE_NEG.
DR      PROSITE; PS00022; EGF_1; 6.
DR      PROSITE; PS01186; EGF_2; 6.
DR      PROSITE; PS50026; EGF_3; 6.
KW      Alternative splicing; Developmental protein; Differentiation;
KW      EGF-like domain; Membrane; Notch signaling pathway; Repeat; Signal;
KW      Transmembrane; Ubl conjugation.
FT      SIGNAL          1          32          Potential.
FT      CHAIN           33         592          Delta-like protein 3.
FT                                         /FTId=PRO_0000007510.
FT      TOPO_DOM        33         490          Extracellular (Potential).
FT      TRANSMEM        491         511          Potential.
FT      TOPO_DOM        512         592          Cytoplasmic (Potential).
FT      DOMAIN          174         213          DSL.
FT      DOMAIN          214         247          EGF-like 1.
FT      DOMAIN          272         308          EGF-like 2.
FT      DOMAIN          310         349          EGF-like 3.
FT      DOMAIN          351         387          EGF-like 4.
FT      DOMAIN          389         425          EGF-like 5.
FT      DOMAIN          427         463          EGF-like 6.
FT      DISULFID        218         229          By similarity.
FT      DISULFID        222         235          By similarity.
FT      DISULFID        237         246          By similarity.
FT      DISULFID        276         287          By similarity.
FT      DISULFID        281         296          By similarity.
FT      DISULFID        298         307          By similarity.
FT      DISULFID        314         325          By similarity.
FT      DISULFID        319         337          By similarity.
FT      DISULFID        339         348          By similarity.
FT      DISULFID        355         366          By similarity.
FT      DISULFID        360         375          By similarity.
FT      DISULFID        377         386          By similarity.
FT      DISULFID        393         404          By similarity.
FT      DISULFID        398         413          By similarity.
FT      DISULFID        415         424          By similarity.
FT      DISULFID        431         442          By similarity.
FT      DISULFID        436         451          By similarity.
FT      DISULFID        453         462          By similarity.
FT      VARSPLIC        585         592          DWLIQVLF -> A (in isoform 1).
FT                                         /FTId=VSP_001376.
FT      CONFLICT        94          94          E -> K (in Ref. 3).
FT      CONFLICT        401         401         G -> A (in Ref. 1).
SQ      SEQUENCE        592 AA;  62069 MW;  1A84F8022E7E7DCC CRC64;

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Query Match 83.6%; Score 2729; DB 1; Length 592;  
Best Local Similarity 82.8%; Pred. No. 1.2e-163;  
Matches 485; Conservative 33; Mismatches 62; Indels 6; Gaps 3;

[illegible]

Db	119	SLVIETWREQLGEHAGGPAWNLLARVVGRRRLAAGGPWARDVQRTGTWELHFSYRARCEP	178
Qy	181	PAVGTACTRLCRPRSAPSRGPGLRPCAPLEDE----SVCRAGCSPEHGFCEQPGECRCL	236
		:   :	
Db	179	PAVGAAACARLCRSRSAPSRGPGLRPCTPFPDECEAPSVCRPGCSPEHGYCEEPDECRL	238
Qy	237	EGWTGPLCTVPVSTSSCLSPRGPSATTGCLVPGPGCDGNPCANGGSCSETPRSFECTC	296
		:      :     :	
Db	239	EGWTGPLCTVPVSTSSCLNSRVPGPASTGCLLPGPGPCDGNPCANGGSCSETSGSFECAC	298
Qy	297	PRGFYGLRCEVSGVTCADGPCFNGLCVGGADPDSAYICHCPPGFQGSNCEKRVDRCSLQ	356
Db	299	PRGFYGLRCEVSGVTCADGPCFNGLCVGGEDPDSAYVCHCPPGFQGSNCEKRVDRCSLQ	358
Qy	357	PCRNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGAHRCSCALG	416
		:	
Db	359	PCQNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCVEGGGSRRCSALG	418
Qy	417	FGGRDCRERADPCAARPCAHGGRCYAHFSGLVACAPGYMGARCEFPVHPDGASALPAAP	476
		:	
Db	419	FGGRDCRERADPCASRPCAHGGRCYAHFSGLVACAPGYMGVRCEFAVRPDGADAVPAAP	478
Qy	477	PGLRPGDPQRYLLPPALGLLVAAGVAGAALLLVHVRRRRGHSQDAGSRLLAGTPEPSVHAL	536
		:                        :             :   :	
Db	479	RGLRQADPQRFLLPPALGLLVAAGLAGAALLVIHVRRRRGPGQDTGTRLLSGTREPSVHTL	538
Qy	537	PDALNNLRTQEGSGDGPSSSVVDWNRPEDVDPQGIYVISAPSIYARE	582
		:                 :	
Db	539	PDALNNLRLQDGAGDGPSSSADWNHPEDGDSRSIYVIPAPSIYARE	584